

HZCYTOR02.SEQ - [REDACTED]  
 Sequence of pcr products generated with 9800-9802,  
 nested pcr product 9941-AP2 (9801-AP1)  
 nested pcr product 9937-AP2 (9803-AP1)  
 Enzyme Recognition Cut Site

AgeI	(A <sup>^</sup> CCGGT)	Def: 1124
BamHI	(G <sup>^</sup> GATCC)	Def: 172
DraI	(TTT <sup>^</sup> AAA)	Def: 36
EcoRI	(G <sup>^</sup> AATTC)	Def: 450
EcoRV	(GAT <sup>^</sup> ATC)	Def: 438
HpaI	(GTT <sup>^</sup> AAC)	Def: 145
MscI	(TGG <sup>^</sup> CCA)	Def: 1244
MunI	(C <sup>^</sup> AATTG)	Def: 493
NcoI	(C <sup>^</sup> CATGG)	Def: 377
NsiI	(ATGCA <sup>^</sup> T)	Def: 592
Ppu10I	(A <sup>^</sup> TGCAT)	Def: 588
SmaI	(CCC <sup>^</sup> GGG)	Def: 11
SspI	(AAT <sup>^</sup> ATT)	Def: 503 988 1107
XmaI	(C <sup>^</sup> CCGGG)	Def: 9

HZCYTOR02.SEQ Linear LENGTH = 1289



This should be the full  
 sequence. The other  
 sequence I gave you had  
 3 mistakes in it.

1 CCCCCCGCCGGGAGAGAGGCAATATCAAGGTTTAAATCTCGGAGAAATGGCTTTCGTTTGGCTGGCT 69  
 GGGGGGCGGGCCTCTCTCCGTATAGTTCCAAAATTTAGAGCCTCTTACCGAAAGCAACGAACCGA  
 11 36 M A F V C L A 7

70 ATCGGATGCTTATATACCTTTCTGATAAGCACAACTTTGGCTGTACTTCATCTTCAGACACCGAGATA 138  
 TAGCCTACGAATATATGGAAGACTATTCGTGTTGTAACCGACATGAAGTAGAAGTCTGTGGCTCTAT  
 I G C L Y T F L I S T T F G C T S S D T E I 30  
 Prod. N-term S25

139 AAAGTTAACCCCTCCTCAGGATTTTGAGATAGTGGATCCCGGATACCTAGGTTATCTCTATTTGCAATGG 207  
 TTTCAATTGGGAGGAGTCTAAACTCTATCACCTAGGGCCTATGAATCCAATAGAGATAAACGTTACC  
 K V N P P Q D F E I V D P G Y L G Y L Y L Q W 53  
 145 172

208 CAACCCCACTGTCTCTGGATCATTTTAAGGAATGCACAGTGAATATGAACATAAATACCGAAACATT 276  
 GTTGGGGGTGACAGAGACCTAGTAAATTCCTTACGTGTACCTTATACCTTATGCTTTTGTAA  
 Q P P L S L D H F K E C T V E Y E L K Y R N I 76

277 GGTAGTGAAACATGGAAGACCATCATTACTAAGAATCTACATTACAAGATGGGTTTGATCTTAACAAG 345  
 CCATCACTTTGTACCTTCTGTAGTAATGATTCTTAGATGTAATGTTTCTACCCAACTAGAATTGTTT  
 G S E T W K T I I T K N L H Y K D G F D L N K 99

346 GGCATTGAAGCGAAGATACACACGCTTTTACCATGGCAATGCACAAATGGATCAGAAGTTCAAAGTTCC 414  
 CCGTAACCTCGCTTCTATGTGTGCGAAATGGTACCGTTACGTGTTTACCTAGTCTTCAAGTTTCAAGG  
 G I E A K I H T L L P W Q C T N G S E V Q S S 122  
 377

415 TGGGCAGAACTACTTATTGGATATCACCACAAGGAATTCAGAACTAAAGTTCAGGATATGGATTGC 483  
 ACCCGTCTTTGATGAATAACCTATAGTGGTTCCTTAAGGTCCTTGAATTCAGTCTATACCTAACG  
 W A E T T Y W I S P Q G I P E T K V Q D M D C 145  
 438 450

484 GSTATATTACAATTGGCAATATTTACTCTGTTCTTGAAACCTGGCATAGGTGTACTTCTTGATACCAAT 552  
 CATATAATGTTAACCGTTATAAATGAGACAAGAACCTTTGGACCGTATCCACATGAAGAATATGGTTA  
 V Y Y N W Q Y L L C S W K P G I G V L L D T N 168  
 493 503

23 a.a/line

maximize 25-380  
 PMD = 23  
 Ek-cell - 25-339  
 PMD 340-363  
 Cyto 364-380



Ppu101  
NsiI

Best Available Copy

Best Available Copy

553 TACAACCTGTTTACTGGTATGAGGGCTTGGATCATGCATTACAGTGTGTTGATTACATCAAGGCTGAT 621  
ATGTTGAACAAAATGACCATACTCCCAACCTAGTACGTAATGTCACAACTAATGTAGTCCGACTA 191  
Y N L F Y W Y E G L D H A L Q C V D Y I K A D  
588 592

622 GGACAAAATATAGGATGCAGATTTCCCTATTTGGAGGCATCAGACTATAAAGATTTCTATATTTGTGT 690  
CCTGTTTATATCTACGTCTAAAGGGATAAACCTCCGTAGTCTGATATTTCTAAAGATATAAACACAA 214  
G Q N I G C R F P Y L E A S D Y K D F Y I C V

691 AATGGATCATCAGAGAACAAGCCTATCAGATCCAGTTATTTCACTTTTCAGCTTCAAAATATAGTTAAA 759  
TTACCTAGTAGTCTCTTGTTCGGATAGTCTAGGTCAATAAAGTGAAAAGTCGAAGTTTATATCAATTT 237  
N G S S E N K P I R S S Y F T E Q L Q N I V K

760 CCTTTGCCGCCAGTCTATCTTACTTTTACTCGGGAGAGTTCATGTGAAATTAAGCTGAAATGGAGCATA 828  
GGAAACGGCGGTGAGATAGAATGAAATGAGCCCTCTCAAGTACACTTTAATTCGACTTTACCTCGTAT 260  
P L P P V Y L T F T R E S S C E I K L K W S I

829 CCTTTGGGACCTATTTCCAGCAAGGTGTTTTGATTATGAAATTGAGATCAGAGAAGATGATACTACCTTG 897  
GGAAACCTGGATAAGGTGCTTCCACAAAATACTTTAATCTAGTCTCTTCTACTATGATGGAAC 283  
P L G P I P A R C F D Y E I E I R E D D T T L

898 GTGACTGCTACAGTTGAAATGAAACATACACCTTGAAAACAACAAATGAAACCCGACAATTATGCTTT 966  
CACTGACGATGTCACTTTTACTTTGTATGTGGAACCTTTTGTGTTTACTTTGGGCTGTTAATACGAAA 306  
V T A T V E N E T Y T L K T T N E T R Q L C F

SspI

967 GTAGTAAGAAGCAAAGTGAATATTTATGCTCAGATGACGGAATTTGGAGTGAGTGGAGTGATAACAA 1035  
CATATTCTTCGTTTCACTTATAAATAACGAGTCTACTGCTTAAACCTCACTCACCTCACTATTTGTT 329  
V V R S K V N I Y C S D D G I W S E W S D K Q  
988

1036 TGCTGGGAAGGTGAAGACCTATCGAAGAAAACCTTTGCTACGTTTCTGGCTACCATTTGGTTTCATCTTA 1104  
ACGACCTTCCACTTCTGGATAGCTTCTTTTGAACGATGCAAAGACCGATGGTAAACCAAAGTAGAAT 352  
C W E G E D L S K K T L L R F W L P F G F I L  
337 TMD

SspI

AgeI

1105 ATATTAGTTATATTTGTAACCGGTCTGCTTTTGGTAAGCCAAACACCTACCCAAAAATGATTCAGAA 1173  
TATAATCAATATAAACATTGGCCAGACGAAAACGCAATTCGGTTTGTGGATGGGTTTTACTAAGGTCTT 375  
I L V I F V T G L L L R K P N T Y P K M I P E  
1107 1124 363

1174 TTTTCTGTGATACATGAAGACTTTCCATATCAAGAGACATGGTATTGACTCAACAGTTTCCAGTCATG 1242  
AAAAAGACACTATGTACTTCTGAAAGGTATAGTTCTGTACCATAACTGAGTTGTCAAAGGTCAGTAC  
F F C D T

MscI

1243 GCCAAATGTTCAATATGAGTCTCAATAAAGTGAATTTTCTTGCGAA 1289  
CGGTTTACAAGTTATCTCAGAGTTATTTGACTTAAAAAGAAGCGCTT

1244

